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(54) Title: ANTI-OBESITY PROTEINS

(57) Abstract

The present invention provides anti-obesity proteins, which when administered to a patient regulate fat tissue. Accordingly, such agents allow patients to overcome their obesity handicap and live normal lives with much reduced risk for type II diabetes, cardiovascular disease and cancer.

Anti-Obesity Proteins

The present invention is in the field of human medicine, particularly in the treatment of obesity and disorders associated with obesity. Most specifically the invention relates to anti-obesity proteins that when administered to a patient regulate fat tissue.

Obesity, and especially upper body obesity, is a common and very serious public health problem in the United States and throughout the world. According to recent statistics, more than 25% of the United States population and 27% of the Canadian population are overweight. Kuczmarski, Amer. J. of Clin. Nutr. 55: 495S - 502S (1992); Reeder et. al., Can. Med. Ass. J., 23: 226-233 (1992). Upper body obesity is the strongest risk factor known for type II diabetes mellitus, and is a strong risk factor for cardiovascular disease and cancer as well. Recent estimates for the medical cost of obesity are $150,000,000,000 world wide. The problem has become serious enough that the surgeon general has begun an initiative to combat the ever increasing adiposity rampant in American society.

Much of this obesity induced pathology can be attributed to the strong association with dyslipidemia, hypertension, and insulin resistance. Many studies have demonstrated that reduction in obesity by diet and exercise reduces these risk factors dramatically. Unfortunately, these treatments are largely unsuccessful with a failure rate reaching 95%. This failure may be due to the fact that the condition is strongly associated with genetically inherited factors that contribute to increased appetite, preference for highly caloric foods, reduced physical activity, and increased lipogenic metabolism. This indicates that people inheriting these genetic traits are prone to becoming obese regardless of their efforts to combat the condition. Therefore, a pharmacological agent that can correct this adiposity handicap and allow the physician to successfully

superior therapeutic agent with improved stability. Accordingly, the present invention provides biologically active obesity proteins. The proteins of the present invention are more readily formulated and stored. Furthermore, the present compounds are more pharmaceutically elegant, which results in superior delivery of therapeutic doses. Thus, such agents allow patients to overcome their obesity handicap and live normal lives with a more normalized risk for type II diabetes, cardiovascular disease and cancer.

Summary of Invention

The present invention is directed to a protein of the Formula (I):

(SEQ.ID NO: 1)

```
Val Pro Ile Xaa Lys Val Xaa Asp Asp Thr Lys Thr Leu Ile Lys Thr
1               5                  10                  15

Ile Val Thr Arg Ile Xaa Asp Ile Ser His Xaa Xaa Ser Val Ser Ser
            20                  25                  30

Lys Xaa Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile
        35                  40                  45

Leu Thr Leu Ser Lys Xaa Asp Xaa Thr Leu Ala Val Tyr Xaa Xaa Ile
    50                  55                  60

Leu Thr Ser Xaa Pro Ser Arg Xaa Val Ile Xaa Ile Xaa Xaa Asp Leu
65                  70                  75                  80

Glu Xaa Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys
                85                  90                  95

His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly
            100                 105                 110

Val Leu Glu Ala Ser Xaa Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
        115                 120                 125

Leu Xaa Gly Ser Leu Xaa Asp Xaa Leu Trp Xaa Leu Asp Leu Ser Pro
    130                 135                 140

145
Gly Cys                                                        (I)
```

wherein:

Xaa at position 4 is Gln or Glu;

Xaa at position 7 is Gln or Glu;

Gly at position 111 is replaced with Asp; or

Trp at position 138 is replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu;

or a pharmaceutically acceptable salt thereof.

The invention further provides a method of treating obesity, which comprises administering to a mammal in need thereof a protein of the Formula (I).

The invention further provides a pharmaceutical formulation, which comprises a protein of the Formula (I) together with one or more pharmaceutically acceptable diluents, carriers or excipients therefor.

An additional embodiment of the present invention is a process for producing a protein of Formula (I), which comprises:

(a) transforming a host cell with DNA that encodes the protein of Formula (I), said protein having an optional leader sequence;

(b) culturing the host cell and isolating the protein encoded in step (a); and, optionally,

(c) cleaving enzymatically the leader sequence to produce the protein of Formula (I).

Detailed Description

For purposes of the present invention, as disclosed and claimed herein, the following terms and abbreviations are defined as follows:

Base pair (bp) -- refers to DNA or RNA. The abbreviations A,C,G, and T correspond to the 5'-monophosphate forms of the nucleotides (deoxy)adenine, (deoxy)cytidine, (deoxy)guanine, and (deoxy)thymine, respectively, when they occur in DNA molecules. The abbreviations U,C,G, and T correspond to the 5'-monophosphate forms of the nucleosides uracil, cytidine, guanine, and thymine, respectively when they occur in RNA molecules. In double stranded DNA, base

Recombinant DNA Expression Vector -- any recombinant DNA cloning vector in which a promoter has been incorporated.

Replicon -- A DNA sequence that controls and allows for autonomous replication of a plasmid or other vector.

RNA -- ribonucleic acid.

RP-HPLC -- an abbreviation for reversed-phase high performance liquid chromatography.

Transcription -- the process whereby information contained in a nucleotide sequence of DNA is transferred to a complementary RNA sequence.

Translation -- the process whereby the genetic information of messenger RNA is used to specify and direct the synthesis of a polypeptide chain.

Tris -- an abbreviation for tris(hydroxymethyl)-aminomethane.

Treating -- describes the management and care of a patient for the purpose of combating the disease, condition, or disorder and includes the administration of a compound of present invention to prevent the onset of the symptoms or complications, alleviating the symptoms or complications, or eliminating the disease, condition, or disorder. Treating obesity therefor includes the inhibition of food intake, the inhibition of weight gain, and inducing weight loss in patients in need thereof.

Vector -- a replicon used for the transformation of cells in gene manipulation bearing polynucleotide sequences corresponding to appropriate protein molecules which, when combined with appropriate control sequences, confer specific properties on the host cell to be transformed. Plasmids, viruses, and bacteriophage are suitable vectors, since they are replicons in their own right. Artificial vectors are constructed by cutting and joining DNA molecules from different sources using restriction enzymes and ligases. Vectors include Recombinant DNA cloning vectors and Recombinant DNA expression vectors.

Asn at position 22 is optionally Gln or Asp;
Thr at position 27 is optionally Ala;
Gln at position 28 is optionally Glu or absent;
Met at position 54 is optionally Ala;
Met at position 68 is optionally Leu;
Asn at position 72 is optionally Glu, or Asp;
Ser at position 77 is optionally Ala;
Gly at position 118 is optionally Leu;

said protein having at least one substitution selected from the group consisting of:

His at position 97 is replaced with Gln, Asn, Ala, Gly, Ser, or Pro;
Trp at position 100 is replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu;
Ala at position 101 is replaced with Ser, Asn, Gly, His, Pro, Thr, or Val;
Ser at position 102 is replaced with Arg;
Gly at position 103 is replaced with Ala;
Glu at position 105 is replaced with Gln;
Thr at position 106 is replaced with Lys or Ser;
Leu at position 107 is replaced with Pro;
Asp at position 108 is replaced with Glu;
Gly at position 111 is replaced with Asp; or
Trp at position 138 is replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu;

or a pharmaceutically acceptable salt thereof.

Preferred proteins are of the Formula II, wherein: Trp at position 100 is Gln, Tyr, Phe, Ile, Val, or Leu; or Trp at position 138 is Gln, Tyr, Phe, Ile, Val, or Leu.

Other preferred proteins of the Formula III:

(SEQ ID NO: 3)

5 10 15
Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr

Most preferred proteins are those of Formula III, wherein:

His at position 97 is replaced with Gln, Asn, Ala, Gly, Ser, or Pro;

Trp at position 100 is replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu;

Ala at position 101 is replaced with Ser, Asn, Gly, His, Pro, Thr or Val;

Glu at position 105 is replaced with Gln;

Thr at position 106 is replaced with Lys or Ser;

Leu at position 107 is replaced with Pro;

Asp at position 108 is replaced with Glu;

Gly at position 111 is replaced with Asp; or

Trp at position 138 is Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu.

Still more preferred proteins of the Formula III are those wherein:

His at position 97 is replaced with Ser or Pro;

Trp at position 100 is replaced with Ala, Gly, Gln, Val, Ile, or Leu;

Ala at position 101 is replaced with Thr; or

Trp at position 138 is Ala, Ile, Gly, Gln, Val or Leu.

Additional preferred proteins of the Formula III are those wherein:

His at position 97 is replaced with Ser or Pro;

Trp at position 100 is replaced with Ala, Gln or Leu;

Ala at position 101 is replaced with Thr; or

Trp at position 138 is Gln.

Additional preferred proteins of the present invention include proteins of SEQ ID NO: 3, wherein the amino acid residues at positions 97, 100, 101, 105, 106, 107, 108, and 111 are substituted as follows in Table 1:

33	His	Trp	Ala	Glu	Lys	Leu	Asp	Asp
34	His	Trp	Ala	Glu	Thr	Pro	Glu	Gly
35	His	Trp	Ala	Glu	Thr	Pro	Asp	Asp
36	His	Trp	Ala	Glu	Thr	Leu	Glu	Asp
37	Ser	Gln	Thr	Glu	Thr	Leu	Asp	Gly
38	Ser	Gln	Ala	Gln	Thr	Leu	Asp	Gly
39	Ser	Gln	Ala	Glu	Lys	Leu	Asp	Gly
40	Ser	Gln	Ala	Glu	Thr	Pro	Asp	Gly
41	Ser	Gln	Ala	Glu	Thr	Leu	Glu	Gly
42	Ser	Gln	Ala	Glu	Thr	Leu	Asp	Asp
43	Ser	Trp	Thr	Gln	Thr	Leu	Asp	Gly
44	Ser	Trp	Thr	Glu	Lys	Leu	Asp	Gly
45	Ser	Trp	Thr	Glu	Thr	Pro	Asp	Gly
46	Ser	Trp	Thr	Glu	Thr	Leu	Glu	Gly
47	Ser	Trp	Thr	Glu	Thr	Leu	Asp	Asp
48	Ser	Trp	Ala	Gln	Lys	Leu	Asp	Gly
49	Ser	Trp	Ala	Gln	Thr	Pro	Asp	Gly
50	Ser	Trp	Ala	Gln	Thr	Leu	Glu	Gly
51	Ser	Trp	Ala	Gln	Thr	Leu	Asp	Asp
52	Ser	Trp	Ala	Glu	Lys	Pro	Asp	Gly
53	Ser	Trp	Ala	Glu	Lys	Leu	Glu	Gly
54	Ser	Trp	Ala	Glu	Lys	Leu	Asp	Asp
55	Ser	Trp	Ala	Glu	Thr	Pro	Glu	Gly
56	Ser	Trp	Ala	Glu	Thr	Pro	Asp	Asp
57	Ser	Trp	Ala	Glu	Thr	Leu	Glu	Asp
58	His	Gln	Thr	Gln	Thr	Leu	Asp	Gly
59	His	Gln	Thr	Glu	Lys	Leu	Asp	Gly
60	His	Gln	Thr	Glu	Thr	Pro	Asp	Gly
61	His	Gln	Thr	Glu	Thr	Leu	Glu	Gly
62	His	Gln	Thr	Glu	Thr	Leu	Asp	Asp
63	His	Gln	Ala	Gln	Lys	Leu	Asp	Gly
64	His	Gln	Ala	Gln	Thr	Pro	Asp	Gly
65	His	Gln	Ala	Gln	Thr	Leu	Glu	Gly
66	His	Gln	Ala	Gln	Thr	Leu	Asp	Asp
67	His	Gln	Ala	Glu	Lys	Pro	Asp	Gly
68	His	Gln	Ala	Glu	Lys	Leu	Glu	Gly

105	Ser	Gln	Ala	Glu	Thr	Pro	Glu	Gly
106	Ser	Gln	Ala	Glu	Thr	Pro	Asp	Asp
107	Ser	Gln	Ala	Glu	Thr	Leu	Glu	Asp
108	Ser	Trp	Thr	Gln	Lys	Leu	Asp	Gly
109	Ser	Trp	Thr	Gln	Thr	Pro	Asp	Gly
110	Ser	Trp	Thr	Gln	Thr	Leu	Glu	Gly
111	Ser	Trp	Thr	Gln	Thr	Leu	Asp	Asp
112	Ser	Trp	Thr	Glu	Lys	Pro	Asp	Gly
113	Ser	Trp	Thr	Glu	Lys	Leu	Glu	Gly
114	Ser	Trp	Thr	Glu	Lys	Leu	Asp	Asp
115	Ser	Trp	Thr	Glu	Thr	Pro	Glu	Gly
116	Ser	Trp	Thr	Glu	Thr	Pro	Asp	Asp
117	Ser	Trp	Thr	Glu	Thr	Leu	Glu	Asp
118	Ser	Trp	Ala	Gln	Lys	Pro	Asp	Gly
119	Ser	Trp	Ala	Gln	Lys	Leu	Glu	Gly
120	Ser	Trp	Ala	Gln	Lys	Leu	Asp	Asp
121	Ser	Trp	Ala	Gln	Thr	Pro	Glu	Gly
122	Ser	Trp	Ala	Gln	Thr	Pro	Asp	Asp
123	Ser	Trp	Ala	Gln	Thr	Leu	Glu	Asp
124	Ser	Trp	Ala	Glu	Lys	Pro	Glu	Gly
125	Ser	Trp	Ala	Glu	Lys	Pro	Asp	Asp
126	Ser	Trp	Ala	Glu	Lys	Leu	Glu	Asp
127	Ser	Trp	Ala	Glu	Thr	Pro	Glu	Asp
128	His	Gln	Thr	Gln	Lys	Leu	Asp	Gly
129	His	Gln	Thr	Gln	Thr	Pro	Asp	Gly
130	His	Gln	Thr	Gln	Thr	Leu	Glu	Gly
131	His	Gln	Thr	Gln	Thr	Leu	Asp	Asp
132	His	Gln	Thr	Glu	Lys	Pro	Asp	Gly
133	His	Gln	Thr	Glu	Lys	Leu	Glu	Gly
134	His	Gln	Thr	Glu	Lys	Leu	Asp	Asp
135	His	Gln	Thr	Glu	Thr	Pro	Glu	Gly
136	His	Gln	Thr	Glu	Thr	Pro	Asp	Asp
137	His	Gln	Thr	Glu	Thr	Leu	Glu	Asp
138	His	Gln	Ala	Gln	Lys	Pro	Asp	Gly
139	His	Gln	Ala	Gln	Lys	Leu	Glu	Gly
140	His	Gln	Ala	Gln	Lys	Leu	Asp	Asp

177	His	Gln	Thr	Glu	Lys	Pro	Glu	Gly
178	His	Gln	Thr	Gln	Thr	Leu	Glu	Asp
179	His	Gln	Thr	Gln	Thr	Pro	Asp	Asp
180	His	Gln	Thr	Gln	Thr	Pro	Glu	Gly
181	His	Gln	Thr	Gln	Lys	Leu	Asp	Asp
182	His	Gln	Thr	Gln	Lys	Leu	Glu	Gly
183	His	Gln	Thr	Gln	Lys	Pro	Asp	Gly
184	Ser	Trp	Ala	Glu	Lys	Pro	Glu	Asp
185	Ser	Trp	Ala	Gln	Thr	Pro	Glu	Asp
186	Ser	Trp	Ala	Gln	Lys	Leu	Glu	Asp
187	Ser	Trp	Ala	Gln	Lys	Pro	Asp	Asp
188	Ser	Trp	Ala	Gln	Lys	Pro	Glu	Gly
189	Ser	Trp	Thr	Glu	Thr	Pro	Glu	Asp
190	Ser	Trp	Thr	Glu	Lys	Leu	Glu	Asp
191	Ser	Trp	Thr	Glu	Lys	Pro	Asp	Asp
192	Ser	Trp	Thr	Glu	Lys	Pro	Glu	Gly
193	Ser	Trp	Thr	Gln	Thr	Leu	Glu	Asp
194	Ser	Trp	Thr	Gln	Thr	Pro	Asp	Asp
195	Ser	Trp	Thr	Gln	Thr	Pro	Glu	Gly
196	Ser	Trp	Thr	Gln	Lys	Leu	Asp	Asp
197	Ser	Trp	Thr	Gln	Lys	Leu	Glu	Gly
198	Ser	Trp	Thr	Gln	Lys	Pro	Asp	Gly
199	Ser	Gln	Ala	Glu	Thr	Pro	Glu	Asp
200	Ser	Gln	Ala	Glu	Lys	Leu	Glu	Asp
201	Ser	Gln	Ala	Glu	Lys	Pro	Asp	Asp
202	Ser	Gln	Ala	Glu	Lys	Pro	Glu	Gly
203	Ser	Gln	Ala	Gln	Thr	Leu	Glu	Asp
204	Ser	Gln	Ala	Gln	Thr	Pro	Asp	Asp
205	Ser	Gln	Ala	Gln	Thr	Pro	Glu	Gly
206	Ser	Gln	Ala	Gln	Lys	Leu	Asp	Asp
207	Ser	Gln	Ala	Gln	Lys	Leu	Glu	Gly
208	Ser	Gln	Ala	Gln	Lys	Pro	Asp	Gly
209	Ser	Gln	Thr	Glu	Thr	Leu	Glu	Asp
210	Ser	Gln	Thr	Glu	Thr	Pro	Asp	Asp
211	Ser	Gln	Thr	Glu	Thr	Pro	Glu	Gly
212	Ser	Gln	Thr	Glu	Lys	Leu	Asp	Asp

249	Ser	Gln	Ala	Gln	Lys	Pro	Glu	Asp
250	Ser	Gln	Thr	Glu	Lys	Pro	Glu	Asp
251	Ser	Gln	Thr	Gln	Thr	Pro	Glu	Asp
252	Ser	Gln	Thr	Gln	Lys	Leu	Glu	Asp
253	Ser	Gln	Thr	Gln	Lys	Pro	Asp	Asp
254	Ser	Gln	Thr	Gln	Lys	Pro	Glu	Gly
255	Ser	Gln	Thr	Gln	Lys	Pro	Glu	Asp
256	His	Ala	Ala	Glu	Thr	Leu	Asp	Gly
257	His	Leu	Ala	Glu	Thr	Leu	Asp	Gly
258	Pro	Trp	Ala	Glu	Thr	Leu	Asp	Gly

Most preferred species of Formula III and Table 1 include species of SEQ ID NO: 4-11:

(SEQ ID NO: 4)

Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
5 10 15
Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser
20 25 30
Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile
35 40 45
Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile
50 55 60
Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu
65 70 75 80
Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys
85 90 95
His Leu Pro Ala Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly
100 105 110
Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
115 120 125
Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro
130 135 140
Gly Cys
145

(SEQ ID NO: 5)

Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
5 10 15

(SEQ ID NO: 7)

```
                    5                  10                  15
Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
            20                  25                  30
Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser
        35                  40                  45
Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile
    50                  55                  60
Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile
65                  70                  75                  80
Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu
                85                  90                  95
Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys
            100                 105                 110
His Leu Pro Gln Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly
        115                 120                 125
Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
    130                 135                 140
Leu Gln Gly Ser Leu Gln Asp Met Leu Gln Gln Leu Asp Leu Ser Pro
145
Gly Cys
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(SEQ ID NO: 8)

```
                    5                  10                  15
Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
            20                  25                  30
Ile Val Thr Arg Ile Asn Asp Ile Ser His Ala Gln Ser Val Ser Ser
        35                  40                  45
Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile
    50                  55                  60
Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile
65                  70                  75                  80
Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu
                85                  90                  95
Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys
            100                 105                 110
His Leu Pro Ala Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly
        115                 120                 125
Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
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          115                 120                 125
Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg

      130                 135                 140
Leu Gln Gly Ser Leu Gln Asp Met Leu Gln Gln Leu Asp Leu Ser Pro

145
Gly Cys
```

(SEQ ID NO: 11)

```
                5                  10                  15
Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr

            20                  25                  30
Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser

        35                  40                  45
Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile

    50                  55                  60
Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile

65                  70                  75                  80
Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu

                85                  90                  95
Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys

            100                 105                 110
Ser Leu Pro Gln Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly

        115                 120                 125
Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg

    130                 135                 140
Leu Gln Gly Ser Leu Gln Asp Met Leu Gln Gln Leu Asp Leu Ser Pro

145
Gly Cys
```

The present invention provides biologically active proteins that provide effective treatment for obesity. Unexpectedly, the claimed proteins have improved properties due to specific substitutions to the human obesity protein. The claimed proteins are more stable than both the mouse and human obesity protein and, therefore, are superior therapeutic agents.

The claimed proteins ordinarily are prepared by recombinant techniques. Techniques for making substitutional mutations at predetermined sites in DNA having a known

Glu, cyclohexyl
His, benzyloxymethyl
Lys, 2-chlorobenzyloxycarbonyl
Met, sulfoxide
Ser, Benzyl
Thr, Benzyl
Trp, formyl
Tyr, 4-bromo carbobenzoxy

Boc deprotection may be accomplished with trifluoroacetic acid (TFA) in methylene chloride. Formyl removal from Trp is accomplished by treatment of the peptidyl resin with 20% piperidine in dimethylformamide for 60 minutes at 4°C. Met(O) can be reduced by treatment of the peptidyl resin with TFA/dimethylsulfide/conHCl (95/5/1) at 25°C for 60 minutes. Following the above pre-treatments, the peptides may be further deprotected and cleaved from the resin with anhydrous hydrogen fluoride containing a mixture of 10% m-cresol or m-cresol/10% p-thiocresol or m-cresol/p-thiocresol/dimethyl-sulfide. Cleavage of the side chain protecting group(s) and of the peptide from the resin is carried out at zero degrees Centigrade or below, preferably -20°C for thirty minutes followed by thirty minutes at 0°C. After removal of the HF, the peptide/resin is washed with ether. The peptide is extracted with glacial acetic acid and lyophilized. Purification is accomplished by reverse-phase C18 chromatography (Vydac) column in .1% TFA with a gradient of increasing acetonitrile concentration.

One skilled in the art recognizes that the solid phase synthesis could also be accomplished using the FMOC strategy and a TFA/scavenger cleavage mixture.

B. Recombinant Synthesis

The claimed proteins may also be produced by recombinant methods. Recombinant methods are preferred if a high yield is desired. The basic steps in the recombinant production of protein include:

the controlled excision of the signal peptide from the fusion protein construct.

The gene encoding the claimed protein may also be created by using polymerase chain reaction (PCR). The template can be a cDNA library (commercially available from CLONETECH or STRATAGENE) or mRNA isolated from human adipose tissue. Such methodologies are well known in the art (Maniatis, et al. Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York (1989).

b. Direct expression or Fusion protein

The claimed protein may be made either by direct expression or as fusion protein comprising the claimed protein followed by enzymatic or chemical cleavage. A variety of peptidases (e.g. trypsin) which cleave a polypeptide at specific sites or digest the peptides from the amino or carboxy termini (e.g. diaminopeptidase) of the peptide chain are known. Furthermore, particular chemicals (e.g. cyanogen bromide) will cleave a polypeptide chain at specific sites. The skilled artisan will appreciate the modifications necessary to the amino acid sequence (and synthetic or semi-synthetic coding sequence if recombinant means are employed) to incorporate site-specific internal cleavage sites. See e.g., Carter P., Site Specific Proteolysis of Fusion Proteins, Ch. 13 in Protein Purification: From Molecular Mechanisms to Large Scale Processes, American Chemical Soc., Washington, D.C. (1990).

c. Vector Construction

Construction of suitable vectors containing the desired coding and control sequences employ standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and religated in the form desired to form the plasmids required.

To effect the translation of the desired protein, one inserts the engineered synthetic DNA sequence in any of a plethora of appropriate recombinant DNA expression vectors

reference. The gene encoding A-C-B proinsulin described in U.S. patent No. 5,304,493 can be removed from the plasmid pRB182 with restriction enzymes NdeI and BamHI. The genes encoding the protein of the present invention can be inserted into the plasmid backbone on a NdeI/BamHI restriction fragment cassette.

d. Procaryotic expression

In general, procaryotes are used for cloning of DNA sequences in constructing the vectors useful in the invention. For example, E. coli K12 strain 294 (ATCC No. 31446) is particularly useful. Other microbial strains which may be used include E. coli B and E. coli X1776 (ATCC No. 31537). These examples are illustrative rather than limiting.

Prokaryotes also are used for expression. The aforementioned strains, as well as E. coli W3110 (prototrophic, ATCC No. 27325), bacilli such as Bacillus subtilis, and other enterobacteriaceae such as Salmonella typhimurium or Serratia marcescans, and various pseudomonas species may be used. Promoters suitable for use with prokaryotic hosts include the β-lactamase (vector pGX2907 [ATCC 39344] contains the replicon and β-lactamase gene) and lactose promoter systems (Chang et al., Nature, 275:615 (1978); and Goeddel et al., Nature 281:544 (1979)), alkaline phosphatase, the tryptophan (trp) promoter system (vector pATH1 [ATCC 37695] is designed to facilitate expression of an open reading frame as a trpE fusion protein under control of the trp promoter) and hybrid promoters such as the tac promoter (isolatable from plasmid pDR540 ATCC-37282). However, other functional bacterial promoters, whose nucleotide sequences are generally known, enable one of skill in the art to ligate them to DNA encoding the protein using linkers or adaptors to supply any required restriction sites. Promoters for use in bacterial systems also will contain a Shine-Dalgarno sequence operably linked to the DNA encoding protein.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription which may affect mRNA expression. These regions are transcribed as polyadenylated segments in the untranslated portion of the mRNA encoding protein. The 3' untranslated regions also include transcription termination sites.

Expression vectors may contain a selection gene, also termed a selectable marker. Examples of suitable selectable markers for mammalian cells are dihydrofolate reductase (DHFR, which may be derived from the BglII/HindIII restriction fragment of pJOD-10 [ATCC 68815]), thymidine kinase (herpes simplex virus thymidine kinase is contained on the BamHI fragment of vP-5 clone [ATCC 2028]) or neomycin (G418) resistance genes (obtainable from pNN414 yeast artificial chromosome vector [ATCC 37682]). When such selectable markers are successfully transferred into a mammalian host cell, the transfected mammalian host cell can survive if placed under selective pressure. There are two widely used distinct categories of selective regimes. The first category is based on a cell's metabolism and the use of a mutant cell line which lacks the ability to grow without a supplemented media. Two examples are: CHO DHFR$^-$ cells (ATCC CRL-9096) and mouse LTK$^-$ cells (L-M(TK-) ATCC CCL-2.3). These cells lack the ability to grow without the addition of such nutrients as thymidine or hypoxanthine. Because these cells lack certain genes necessary for a complete nucleotide synthesis pathway, they cannot survive unless the missing nucleotides are provided in a supplemented media. An alternative to supplementing the media is to introduce an intact DHFR or TK gene into cells lacking the respective genes, thus altering their growth requirements. Individual cells which were not transformed with the DHFR or TK gene will not be capable of survival in nonsupplemented media.

Press, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York (1989), or Current Protocols in Molecular Biology (1989) and supplements.

Preferred suitable host cells for expressing the vectors encoding the claimed proteins in higher eukaryotes include: African green monkey kidney line cell line transformed by SV40 (COS-7, ATCC CRL-1651); transformed human primary embryonal kidney cell line 293, (Graham, F. L. et al., J. Gen Virol. 36:59-72 (1977), Virology 77:319-329, Virology 86:10-21); baby hamster kidney cells (BHK-21(C-13), ATCC CCL-10, Virology 16:147 (1962)); Chinese hamster ovary cells CHO-DHFR$^-$ (ATCC CRL-9096), mouse Sertoli cells (TM4, ATCC CRL-1715, Biol. Reprod. 23.243-250 (1980)); African green monkey kidney cells (VERO 76, ATCC CRL-1587); human cervical epitheloid carcinoma cells (HeLa, ATCC CCL-2); canine kidney cells (MDCK, ATCC CCL-34); buffalo rat liver cells (BRL 3A, ATCC CRL-1442); human diploid lung cells (WI-38, ATCC CCL-75); human hepatocellular carcinoma cells (Hep G2, ATCC HB-8065); and mouse mammary tumor cells (MMT 060562, ATCC CCL51).

f. Yeast expression

In addition to prokaryotes, eukaryotic microbes such as yeast cultures may also be used. Saccharomyces cerevisiae, or common baker's yeast is the most commonly used eukaryotic microorganism, although a number of other strains are commonly available. For expression in Saccharomyces, the plasmid YRp7, for example, (ATCC-40053, Stinchcomb, et al., Nature 282:39 (1979); Kingsman et al., Gene 7:141 (1979); Tschemper et al., Gene 10:157 (1980)) is commonly used. This plasmid already contains the trp gene which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example ATCC no. 44076 or PEP4-1 (Jones, Genetics 85:12 (1977)).

Suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase (found on plasmid pAP12BD ATCC 53231 and described in U.S. Patent No. 4,935,350, June 19, 1990) or other glycolytic

```
 51  AAAGACAATA GTCACAAGGA TAAATGATAT CTCACACACA CAGTCAGTCT
101  CATCTAAACA GAAAGTCACA GGCTTGGACT TCATACCTGG GCTGCACCCC
151  ATACTGACAT TGTCTAAAAT GGACCAGACA CTGGCAGTCT ATCAACAGAT
201  CTTAACAAGT ATGCCTTCTA GAAACGTGAT ACAAATATCT AACGACCTGG
251  AGAACCTGCG GGATCTGCTG CACGTGCTGG CCTTCTCTAA AAGTTGCCAC
301  TTGCCATGGG CCAGTGGCCT GGAGACATTG GACAGTCTGG GGGGAGTCCT
351  GGAAGCCTCA GGCTATTCTA CAGAGGTGGT GGCCCTGAGC AGGCTGCAGG
401  GGTCTCTGCA AGACATGCTG TGGCAGCTGG ACCTGAGCCC CGGGTGCTAA
451  TAGGATCC
```

The 220 base pair segment extends from the NdeI site to the XbaI site at position 220 within the coding region and is assembled from 7 overlapping oligonucleotides which range in length from between 34 and 83 bases. The 240 base pair segment which extends from the XbaI to the BamHI site is also assembled from 7 overlapping oligonucleotides which range in length from between 57 and 92 bases.

To assemble these fragments, the respective 7 oligonucleotides are mixed in equimolar amounts, usually at concentrations of about 1-2 picomoles per microliters. Prior to assembly, all but the oligonucleotides at the "5" -ends of the segment are phosphorylated in standard kinase buffer with T4 DNA kinase using the conditions specified by the supplier of the reagents. The mixtures are heated to 95 degrees and allowed to cool slowly to room temperature over a period of 1-2 hours to ensure proper annealing of the oligonucleotides. The oligonucleotides are then ligated to each other and into an appropriated cloning vector such as pUC18 or pUC 19 using T4 DNA ligase. The buffers and conditions are those recommended by the supplier of the enzyme. The vector for the 220 base pair fragment is digested with NdeI and XbaI, whereas the vector for the 240 base pair fragment is digested with XbaI and BamHI prior to use. The ligation mixes are used to transform E. coli DH10B cells (commercially available from Gibco/BRL) and the transformed cells are plated on tryptone-yeast (TY) plates containing 100 µg/ml of

Example 3

A DNA sequence encoding a protein represented by Protein 255 in Table 1 with a Met Arg leader sequence was obtained using the plasmid and procedures described in Example 2. The plasmid was digested with PmlI and Bsu36I. A synthetic DNA fragment of the sequence 5'-SEQ ID NO:13:

(SEQ ID NO: 13)

GTGCTGGCCTTCTCTAAAAGTTGCAGCTTGCCACAGTCCAGTGGCCTGCAGAAACCGGAAA
GTCTGGACGGAGTCCTGGAAGCC

annealed with the sequence 5'-SEQ ID NO:14:

(SEQ ID NO: 14)

TGAGGCTTCCAGGACTCCGTCCAGACTTTCCGGTTTCTGCAGGCCACTGGTCTGTGGCAAG
CTGCAACTTTTAGAGAAGGCCAGCAC

was inserted between the PmlI and the Bsu36I sites. Following ligation, transformation and plasmid isolation, the sequence of the synthetic fragment was verified by DNA sequence analysis.

Example 4

A DNA sequence encoding SEQ ID NO: 4 with a Met Arg leader sequence was obtained using the plasmid and procedures described in Example 2. The plasmid was digested with PmlI and Bsu36I. A synthetic DNA fragment of the sequence 5'-SEQ ID NO:15

(SEQ ID NO: 15)

GTGCTGGCCTTCTCTAAAAGTTGCCACTTGCCAGCTGCCAGTGGCCTGGAGACATTGGACA
GTCTGGGGGGAGTCCTGGAAGCC

annealed with the sequence 5'-SEQ ID NO:16:

(SEQ ID NO: 16)

TGAGGCTTCCAGGACTCCCCCCAGACTGTCCAATGTCTCCAGGCCACTGGCAGCTGGCAAG
TGGCAACTTTTAGAGAAGGCCAGCAC

overexpressed protein. Kreuger et al., in Protein Folding, Gierasch and King, eds., pgs 136-142 (1990), American Association for the Advancement of Science Publication No. 89-18S, Washington, D.C. Such protein aggregates must be dissolved to provide further purification and isolation of the desired protein product. Id. A variety of techniques using strongly denaturing solutions such as guanidinium-HCl and/or weakly denaturing solutions such as urea are used to solubilize the proteins. Gradual removal of the denaturing agents (often by dialysis) in a solution allows the denatured protein to assume its native conformation. The particular conditions for denaturation and folding are determined by the particular protein expression system and/or the protein in question.

Example 5

The protein of Example 3 with a Met Arg leader sequence was expressed in E.coli, isolated and folded either by dilution into PBS or by dilution into 8M urea (both containing 5 mM cysteine) and exhaustive dialysis against PBS. Little to no aggregation of protein was seen in either of these procedures. Following final purification of the proteins by size exclusion chromatography the proteins were concentrated to 3-3.5 mg/mL in PBS. Virtually no aggregation of the protein was noted in contrast to the native human protein for which substantial aggregation is noted upon concentration.

Analysis of the proteins by reverse phase HPLC indicated that the human Ob protein eluted at approximately 56.6 % acetonitrile, the mouse protein at 55.8 %, and the titled protein with a Met Arg leader sequence at 53.7 %. Thus, unexpectedly the human with the mouse insert appears to have higher hydrophilicity than either the human or mouse molecules.

chromatography, affinity chromatography, ion exchange and size exclusion chromatography.

The claimed proteins contain two cysteine residues. Thus, a di-sulfide bond may be formed to stabilize the protein. The present invention includes proteins of the Formula (I) or (II) wherein the Cys at position 96 is crosslinked to Cys at position 146 as well as those proteins without such di-sulfide bonds. In addition the proteins of the present invention may exist, particularly when formulated, as dimers, trimers, tetramers, and other multimers. Such multimers are included within the scope of the present invention.

The present invention provides a method for treating obesity. The method comprises administering to the organism an effective amount of anti-obesity protein in a dose between about 1 and 1000 µg/kg. A preferred dose is from about 10 to 100 µg/kg of active compound. A typical daily dose for an adult human is from about 0.5 to 100 mg. In practicing this method, compounds of the Formula (I) can be administered in a single daily dose or in multiple doses per day. The treatment regime may require administration over extended periods of time. The amount per administered dose or the total amount administered will be determined by the physician and depend on such factors as the nature and severity of the disease, the age and general health of the patient and the tolerance of the patient to the compound.

The instant invention further provides pharmaceutical formulations comprising compounds of the present invention. The proteins, preferably in the form of a pharmaceutically acceptable salt, can be formulated for parenteral administration for the therapeutic or prophylactic treatment of obesity. For example, compounds of the Formula (I) can be admixed with conventional pharmaceutical carriers and excipients. The compositions comprising claimed proteins contain from about 0.1 to 90% by weight of the active protein, preferably in a soluble form, and more generally

agent of similar composition in the same animal monitoring the same parameters or the active agent itself in animals that are thought to lack the receptor (db/db mice, fa/fa or cp/cp rats). Proteins demonstrating activity in these models will demonstrate similar activity in other mammals, particularly humans.

Since the target tissue is expected to be the hypothalamus where food intake and lipogenic state are regulated, a similar model is to inject the test article directly into the brain (e.g. i.c.v. injection via lateral or third ventricles, or directly into specific hypothalamic nuclei (e.g. arcuate, paraventricular, perifornical nuclei). The same parameters as above could be measured, or the release of neurotransmitters that are known to regulate feeding or metabolism could be monitored (e.g. NPY, galanin, norepinephrine, dopamine, β-endorphin release).

Representative proteins outlined in Table 2 were prepared in accordance with the teachings and examples provided herein. The description of the protein in Table 2, and in subsequent Table 3, designates the substituted amino acids of SEQ ID NO: 3 as provided in Formula I. For example, Ala(100) designates a protein of SEQ ID NO: 3 wherein Trp at position 100 is Ala. The designation Met Arg - indicates that the protein was prepared and tested with the Met Arg leader sequence attached. Amino acid sequences of the proteins of Table 2 and 3 were confirmed by mass spectroscopy and/or amino acid analysis. The ability of the present proteins to treat obesity in a *OB/OB* mouse is also presented in Table 2.

Protein	Dose (µg)	route	Food Intake g/mouse				Food Intake % Control			Body Weight Change from 0-time		
			DAY 1	DAY 2	DAY 3		DAY 1	DAY 2	DAY 3	BW∆1	BW∆2	BW∆3
Met-Arg-(Lys106,	300	SC	5.0	4.0	4.0		65.8	52.6	52.6	0.2	-0.2	-0.9
Pro107,Glu108,Arg111)	30	SC	5.4	5.4	5.1		71.1	71.1	67.1	-0.1	0.0	-0.3
(Ser97,Gln100)	300	SC	2.1	1.6	1.3		39.6	30.2	24.5	-1.0	-2.0	-2.7
	30	SC	3.7	3.3	2.9		69.8	62.3	54.7	-0.5	-0.7	-1.1
(Ser97)	300	SC	3.4	2.8	2.6		64.2	52.8	49.1	-0.6	-1.4	-1.4
	30	SC	3.5	3.4	2.8		66.0	64.2	52.8	-0.7	-1.2	-1.7
Met-Arg-(Ala100)	300	SC	4.1	3.1	2.4		78.8	59.6	46.2	-0.7	-1.1	-1.7
	30	SC	3.7	3.1	3.9		71.2	65.4	75.0	-0.1	-0.5	-0.5
Met-Arg-(Ser97)	300	SC	5.6	4.2	2.6		107.7	80.8	50.0	0.0	-0.5	-1.0
	30	SC	5.2	4.5	4.3		100.0	86.5	82.7	0.1	0.0	0.0
(Ser97,Gln100,Thr101)	300	SC	4.4	3.6	2.4		86.3	70.6	47.1	-0.6	-0.4	-1.4
	30	SC	3.8	3.5	3.0		74.5	68.6	58.8	-0.3	-0.3	-0.6
(Ala100)	300	SC	4.5	3.2	2.3		70.3	50.0	35.9	-0.5	-1.1	-1.1
	100	SC	4.6	3.2	3.1		71.9	50.0	48.4	-0.6	-1.4	-1.4
	70	SC	5.6	5.0	4.6		87.5	78.1	71.9	-0.4	-0.8	-0.8

and then closed with the Teflon-coated seal and screw cap. A separate vial is used for each shake test time period that is to be evaluated.

The test vials are placed in a rotation device in an incubator set precisely at 40°C. The vials are rotated end-over-end at a rate of 30 revolutions per minute, allowing the Teflon beads to move gently from the top of the vial to the bottom while remaining completely in the solution.

After pre-determined time periods, the contents of the vials are removed and centrifuged 5 minutes at ambient temperature (Fisher Scientific Model 235C Centrifuge). The protein concentrations in the clear supernatants are determined again by the UV absorbence or SEC techniques. The percent of Ob protein remaining in solution is calculated from the Ob concentrations in the pH-adjusted starting solutions and in the supernatants after the shake test.

The chemical and physical stability of the present compounds is demonstrated in Table 3. The description of the protein in Table 3 designates the substituted amino acids of SEQ ID NO: 3 as provided in Formula (I). For example, Ala(100) designates a protein of SEQ ID NO: 3 wherein Trp at position 100 is replaced with Ala. For reference the human Ob protein and the mouse ob protein are also presented.

Table 3

Protein	mg/mL	Temp	rpm	pH	Time (hrs.)	Percent Remaining
Human	1.6	40	30	5	7	44.7
				5	47	36.6
				6	7	63.4
				6	47	56.9
				7	7	98.6
				7	47	93.7
				8	7	99.9
				8	47	95.9
Mouse	1.6	40	30	5	47	73.5
				6	47	94.9
				7	47	67.4
				8	47	31.6

Met-Arg-(Pro97)	1.6	40	30	5	47	22.4
				6	47	33.8
				7	47	48.1
				8	47	54.8
Met-Arg-(Ala27, Gln100)	1.6	40	30	5	47	93.8
				6	47	87.2
				7	47	96.7
				8	47	98.0
Met-Arg-(Ala27, Leu100)	1.6	40	30	5	47	57.8
				6	47	49.3
				7	47	69.3
				8	47	93.3

The compounds are active in at least one of the above biological tests and are anti-obesity agents. As such, they are useful in treating obesity and those disorders implicated by obesity. However, the proteins are not only useful as therapeutic agents; one skilled in the art recognizes that the proteins are useful in the production of antibodies for diagnostic use and, as proteins, are useful as feed additives for animals. Furthermore, the compounds are useful for controlling weight for cosmetic purposes in mammals. A cosmetic purpose seeks to control the weight of a mammal to improve bodily appearance. The mammal is not necessarily obese. Such cosmetic use forms part of the present invention.

The principles, preferred embodiments and modes of operation of the present invention have been described in the foregoing specification. The invention which is intended to be protected herein, however, is not to be construed as limited to the particular forms disclosed, since they are to be regarded as illustrative rather than restrictive. Variations and changes may be made by those skilled in the art without departing from the spirit of the invention.

Xaa at position 75 is Gln or Glu;
Xaa at position 77 is Ser or Ala;
Xaa at position 78 is Gln, Asn, or Asp;
Xaa at position 82 is Gln, Asn, or Asp;
Xaa at position 118 is Gly or Leu;
Xaa at position 130 is Gln or Glu;
Xaa at position 134 is Gln or Glu;
Xaa at position 136 is Met, methionine sulfoxide, Leu, Ile, Val, Ala, or Gly;
Xaa at position 139 is Gln or Glu;
said protein having at least one substitution selected from the group consisting of:
His at position 97 is replaced with Gln, Asn, Ala, Gly Ser, or Pro;
Trp at position 100 is replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu;
Ala at position 101 is replaced with Ser, Asn, Gly, His, Pro, Thr, or Val;
Ser at position 102 is replaced with Arg;
Gly at position 103 is replaced with Ala;
Glu at position 105 is replaced with Gln;
Thr at position 106 is replaced with Lys or Ser;
Leu at position 107 is replaced with Pro;
Asp at position 108 is replaced with Glu; or
Gly at position 111 is replaced with Asp
Trp at position 138 is replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu;

or a pharmaceutically acceptable salt thereof.

2. A protein of Claim 1 having at least one substitution selected from the group consisting of:
His at position 97 is replaced with Gln, Asn, Ala, Gly, Ser or Pro;
Trp at position 100 is replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln or Leu;

Met at position 68 is optionally Leu;
Asn at position 72 is optionally Glu, or Asp;
Ser at position 77 is optionally Ala;
Gly at position 118 is optionally Leu;

said protein having at least one substitution selected from the group consisting of:

His at position 97 is replaced with Gln, Asn, Ala, Gly, Ser, or Pro;

Trp at position 100 is replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu;

Ala at position 101 is replaced with Ser, Asn, Gly, His, Pro, Thr, or Val;

Ser at position 102 is replaced with Arg;

Gly at position 103 is replaced with Ala;

Glu at position 105 is replaced with Gln;

Thr at position 106 is replaced with Lys or Ser;

Leu at position 107 is replaced with Pro;

Asp at position 108 is replaced with Glu;

Gly at position 111 is replaced with Asp;

Trp at position 138 is replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu;

or a pharmaceutically acceptable salt thereof.

4. A protein of Claim 3, wherein:
Trp at position 100 is Gln, Tyr, Phe, Ile, Val, or Leu; or
Trp at position 138 is Gln, Tyr, Phe, Ile, Val, or Leu.

5. A protein of the Formula III:

(SEQ ID NO: 3)

```
                5                   10                  15
Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr

            20                  25                  30
Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser

        35                  40                  45
Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile
```

Trp at position 100 is replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu;

Ala at position 101 is replaced with Ser, Asn, Gly, His, Pro, Thr or Val;

Glu at position 105 is replaced with Gln;

Thr at position 106 is replaced with Lys or Ser;

Leu at position 107 is replaced with Pro;

Asp at position 108 is replaced with Glu;

Gly at position 111 is replaced with Asp; or

Trp at position 138 is Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu.

7. A protein of Claim 6, wherein:

His at position 97 is replaced with Ser or Pro;

Trp at position 100 is replaced with Ala, Gly, Gln, Val, Ile, or Leu;

Ala at position 101 is replaced with Thr; or

Trp at position 138 is Ala, Ile, Gly, Gln, Val or Leu.

8. A protein of any one of Claim 1 through 7, wherein the Cys at position 96 is di-sulfide bonded to the Cys at position 146.

9. A protein of SEQ ID NO: 4:

(SEQ ID NO: 4)

```
                5                  10                  15
Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr

            20                  25                  30
Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser

        35                  40                  45
Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile

    50                  55                  60
Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile

65                  70                  75                  80
Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu

                85                  90                  95
Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys

            100                 105                 110
```

Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr

20 25 30

Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser

35 40 45

Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile

50 55 60

Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile

65 70 75 80

Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu

85 90 95

Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys

100 105 110

His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly

115 120 125

Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg

130 135 140

Leu Gln Gly Ser Leu Gln Asp Met Leu Gln Gln Leu Asp Leu Ser Pro

145

Gly Cys

wherein the Cys at position 96 is di-sulfide bonded to the Cys at position 146;

or a pharmaceutically acceptable salt thereof.

12. A protein of SEQ ID NO: 7:

(SEQ ID NO: 7)

5 10 15

Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr

20 25 30

Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser

35 40 45

Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile

50 55 60

Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile

65 70 75 80

Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu

85 90 95

Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys

100 105 110

His Leu Pro Gln Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly

115 120 125

Ser Ser Lys Xaa Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His
35 40 45

Pro Ile Leu Thr Leu Ser Lys Xaa Asp Xaa Thr Leu Ala Val Tyr Xaa
50 55 60

Xaa Ile Leu Thr Ser Xaa Pro Ser Arg Xaa Val Ile Xaa Ile Xaa Xaa
65 70 75

Asp Leu Glu Xaa Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys
80 85 90

Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu
95 100 105 110

Gly Gly Val Leu Glu Ala Ser Xaa Tyr Ser Thr Glu Val Val Ala Leu
115 120 125

Ser Arg Leu Xaa Gly Ser Leu Xaa Asp Xaa Leu Trp Xaa Leu Asp Leu
130 135 140

Ser Pro Gly Cys
145

wherein:

R^1 is any amino acid except Pro;

Xaa at position 4 is Gln or Glu;

Xaa at position 7 is Gln or Glu;

Xaa at position 22 is Asn, Asp or Glu;

Xaa at position 27 is Thr or Ala;

Xaa at position 28 is Gln, Glu, or absent;

Xaa at position 34 is Gln or Glu;

Xaa at position 54 is Met, methionine sulfoxide, Leu, Ile, Val, Ala, or Gly;

Xaa at position 56 is Gln or Glu;

Xaa at position 62 is Gln or Glu;

Xaa at position 63 is Gln or Glu;

Xaa at position 68 is Met, methionine sulfoxide, Leu, Ile, Val, Ala, or Gly;

Xaa at position 72 is Asn, Asp or Glu;

Xaa at position 75 is Gln or Glu;

Xaa at position 77 is Ser or Ala;

Xaa at position 78 is Gln, Asn, or Asp;

Xaa at position 82 is Gln, Asn, or Asp;

Xaa at position 118 is Gly or Leu;

17. The process of Claim 16, wherein the leader sequence is Met-R_1-.

18. The process of Claim 17, wherein the leader sequence is Met-Arg-.

19. A pharmaceutical formulation, which comprises a protein as claimed in any one of Claims 1 through 13 together with one or more pharmaceutically acceptable diluents, carriers or excipients therefor.

20. A method of treating obesity, which comprises administering to a mammal in need thereof a protein as claimed in any one of Claims 1 through 13.

21. A protein of any one of Claims 1 through 13 for use as a pharmaceutical agent.

INTERNATIONAL SEARCH REPORT

Inte...nal application No.
PCT/US96/00952

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Methods in Enzymology, Volume 68, issued 1979, Brown et al, "Chemical Synthesis and Cloning of Tyrosine tRNA Gene, pages 109-151, see entire document.	16-18